

O'Bryen, Barbara

From: Angell, Jon E
Sent: Wednesday, June 02, 2004 4:42 PM
To: O'Bryen, Barbara
Subject: Sequence Database Search Request

SEARCH REQUEST FORM
Scientific and Technical Information Center

Examiner# : 78697
Art Unit : 1635
Phone Number: 571-272-0756
Date: 6/2/04
Serial Number: 09/945,173 (Meyers)
Mailbox & Bldg/Room Location: REMSEN 2C18
Results Format Preferred: DISK

I would like to have the following searches performed using the following SEQ. ID NOs. from application : 09/945,173 (Meyers)

SEQ ID NO. 1--nucleic acid sequence (size=~1694 nucleotides)
Please perform: (1) a standard search of SEQ ID NO. 1, as well as
(2) a search that identifies hits that match SEQ ID NO. 1, but are no longer than 50 nucleotides in length
(i.e., size limit search wherein the size limit is set to 50 nucleotides)

SEQ ID NO. 2--amino acid sequence encoded by SEQ ID NO. 1 (size=~236 amino acids)
Please perform a search to identify all nucleic acids which encode the amino acid sequence of SEQ ID NO. 2 (i.e., reverse transcribe & search)

Thanks,
Eric

J. Eric Angell
Art Unit 1635
Office: REMSEN 2D20
mailbox: REM 2C18
571-272-0756

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 19:53:35 ; Search time 6429 Seconds
(without alignments)
11420.610 Million cell

updates/sec

Title: US-09-945-173-1
Perfect score: 1694
Sequence: 1 agggaaggcagtggaagat.....aaacatgaattattgaacta
1694

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: gb_vi:*
15: em_ba:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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sapi						
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sapi						
5	1660.8	98.0	3352	9	HSM807810	BX647664 Homo
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sapi						
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sapi						
8	1022.2	60.3	146010	9	AC009289	AC009289 Homo
sapi						
9	875.6	51.7	2064	10	BC050194	BC050194 Mus
muscu						
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Danio rer						
12	374.8	22.1	385	6	BD076273	BD076273 5'
EST of						
c 13	330.8	19.5	155418	2	AC117754	AC117754 Mus
muscu						
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15	321	18.9	321	6	BD041691	BD041691
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17	301.8	17.8	266597	2	AC119722	AC119722
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muscu						

19	135	8.0	119730	9	AC117472	AC117472 Homo
sapi						
20	135	8.0	188485	2	AC027454	AC027454 Homo
sapi						
c 21	102.2	6.0	165836	2	AC138153	AC138153
Danio rer						
22	102.2	6.0	175167	2	BX571724	BX571724
Danio rer						
c 23	102.2	6.0	180928	2	AC139727	AC139727
Danio rer						
c 24	92.6	5.5	66009	2	AC101250	AC101250 Mus
muscu						
c 25	81.6	4.8	87017	2	AC140043	AC140043 Mus
muscu						
c 26	77.6	4.6	29949	2	AC112488	AC112488 Homo
sapi						
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Macaca mu						
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sapi						
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(2 of						
41	46.8	2.8	84550	3	PFMAL1P2_3	Continuation
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ALIGNMENTS

RESULT 1
AX465669

LOCUS AX465669 1694 bp DNA linear PAT 16-JUL-2002

DEFINITION Sequence 1 from Patent WO0218425.

ACCESSION AX465669

VERSION AX465669.1 GI:21899929

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Meyers, R.A.

TITLE 47324, a human g-protein and uses therefor

JOURNAL Patent: WO 0218425-A 1 07-MAR-2002;

Millennium Pharmaceuticals (US)

FEATURES

Location/Qualifiers

source

1..1694

/organism="Homo sapiens"

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CDS

19..729

/note="unnamed protein product"

/codon_start=1

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ORIGIN

Query Match 100.0%; Score 1694; DB 6; Length 1694;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1694; Conservative 0; Mismatches 0; Indels 0;

Gaps 0;

Qy 1

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Qy 61

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|||||

Db 61

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Qy 121

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Db 121
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Qy 181
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 Db 301
 CACGACTTAACAAATAAGAAGTCCTCCCAAACTTGCGTCGTTGGTCATTGGAAGCTCTC 360

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Qy 1561
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Qy 1621
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Qy 1681 GAATTATTGAACTA 1694

Db 1681 GAATTATTGAACTA 1694

RESULT 2
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 LOCUS HSM807705 3362 bp mRNA linear PRI 30-
 AUG-2003
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 ACCESSION BX647559
 VERSION BX647559.1 GI:34366716
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3362)
 AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C.,
 Osanger,A.,
 Fobo,G., Han,M. and Wiemann,S.
 CONSRTM The German Human cDNA Consortium
 TITLE Direct Submission
 JOURNAL Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-
 85764
 Neuherberg, GERMANY
 COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German
 Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by BMFZ (Biomedical Research Center at the
 Heinrich-Heine-University, Duesseldorf/Germany) within the
 cDNA
 sequencing consortium of the German Genome Project. This
 clone
 (DKFZp313A1611) is available at the RZPD in Berlin. Please
 contact
 the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
 information about the clone and the sequencing project is
 available
 at <http://mips.gsf.de/proj/cdna/>.
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Qy 181
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Qy 301
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 Db 310
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Qy 361
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Qy 541

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Db 550

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Db 610

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Qy 661

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Qy 721

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Qy 781

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Qy 841

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Db 850

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Qy 1021

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Db 1030

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 21:11:55 ; Search time 6428 Seconds
(without alignments)
11422.386 Million cell

updates/sec

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1694

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1603530

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
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26: em_ro:*
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29: em_vi:*

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30: em_htg_hum:*
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41: em_htgo_other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	23	1.4	50	6	AR095375	AR095375
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Arabidops						
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Sequence						
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Sequence						
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Archaeogl						
6	21.8	1.3	41	6	AX515661	AX515661
Sequence						
7	21.8	1.3	41	6	AX518256	AX518256
Sequence						
8	21.8	1.3	47	6	AR291554	AR291554
Sequence						
9	21.6	1.3	42	10	MMU232767	AJ232767 Mus
muscu						
10	21.2	1.3	39	6	AR022583	AR022583
Sequence						
11	21.2	1.3	39	6	AR037598	AR037598
Sequence						
12	21.2	1.3	39	6	AR166584	AR166584
Sequence						
13	21.2	1.3	39	6	AR178056	AR178056
Sequence						
14	21.2	1.3	47	6	AR291096	AR291096
Sequence						
15	20.8	1.2	36	6	AR152139	AR152139
Sequence						
16	20.8	1.2	36	6	AR174546	AR174546
Sequence						
17	20.8	1.2	36	6	AR404212	AR404212
Sequence						
18	20.8	1.2	44	6	AX497105	AX497105
Sequence						

19	20.8	1.2	46	6	I22397	I22397
Sequence 5						
c 20	20.8	1.2	47	6	AR291749	AR291749
Sequence						
21	20.8	1.2	48	9	S64862S2	S64863 alpha
1-the						
22	20.4	1.2	40	6	AR163454	AR163454
Sequence						
23	20.4	1.2	40	6	BD103192	BD103192 O-
fucosyl						
24	20.4	1.2	40	6	BD103194	BD103194 O-
fucosyl						
25	20.4	1.2	45	10	MMC1RNA	X60845
M.musculus						
c 26	20.4	1.2	47	6	AR288610	AR288610
Sequence						
c 27	20.4	1.2	47	6	AX378249	AX378249
Sequence						
c 28	20.4	1.2	47	6	AX378272	AX378272
Sequence						
29	20.4	1.2	50	6	AR423115	AR423115
Sequence						
30	20.4	1.2	50	6	BD118668	BD118668 EST
and e						
31	20.2	1.2	50	6	I36502	I36502
Sequence 1						
32	20.2	1.2	50	6	AR423218	AR423218
Sequence						
c 33	20.2	1.2	50	6	AX261361	AX261361
Sequence						
34	20.2	1.2	50	6	BD118771	BD118771 EST
and e						
c 35	20.2	1.2	50	6	BD170451	BD170451
Method of						
c 36	20	1.2	28	6	AR014037	AR014037
Sequence						
c 37	20	1.2	28	6	I21987	I21987
Sequence 73						
38	20	1.2	39	6	AR302247	AR302247
Sequence						
39	20	1.2	39	6	AR367377	AR367377
Sequence						
40	20	1.2	39	6	AX080330	AX080330
Sequence						
41	20	1.2	47	6	I11814	I11814
Sequence 3						
42	20	1.2	47	6	BD196579	BD196579
Prostatic						
43	20	1.2	50	6	AX164928	AX164928
Sequence						
44	20	1.2	50	8	ATH527926	AJ527926
Arabidops						
c 45	19.8	1.2	45	6	A67371	A67371
Sequence 12						

ALIGNMENTS

RESULT 1
AR095375